

| Ref # | Hits | Search Query                              | DBs   | Default Operator | Plurals | Time Stamp       |
|-------|------|---|---|------------------|---------|------------------|
| L1    | 3    | PLAG1 and CTNNB1                          | US-PGPUB;<br>USPAT;<br>USOCR;<br>EPO; JPO;<br>DERWENT;<br>IBM_TDB | OR               | ON      | 2005/06/15 18:37 |
| L2    | 17   | PLAG1                                     | US-PGPUB;<br>USPAT;<br>USOCR;<br>EPO; JPO;<br>DERWENT;<br>IBM_TDB | OR               | ON      | 2005/06/15 18:38 |
| L3    | 50   | CTNNB1 and (cancer\$3 tumor\$3)           | US-PGPUB;<br>USPAT;<br>USOCR;<br>EPO; JPO;<br>DERWENT;<br>IBM_TDB | OR               | ON      | 2005/06/15 18:38 |
| L4    | 1    | I3 and (CTNNB1 near5 fus\$3)              | US-PGPUB;<br>USPAT;<br>USOCR;<br>EPO; JPO;<br>DERWENT;<br>IBM_TDB | OR               | ON      | 2005/06/15 18:39 |
| L5    | 1    | (CTNNB1 near5 fus\$3)                     | US-PGPUB;<br>USPAT;<br>USOCR;<br>EPO; JPO;<br>DERWENT;<br>IBM_TDB | OR               | ON      | 2005/06/15 18:39 |
| L6    | 21   | (beta adj1 catenin) near5 fus\$3          | US-PGPUB;<br>USPAT;<br>USOCR;<br>EPO; JPO;<br>DERWENT;<br>IBM_TDB | OR               | ON      | 2005/06/15 18:40 |
| L7    | 14   | ((beta adj1 catenin) CTNNB1) near5 (exon) | US-PGPUB;<br>USPAT;<br>USOCR;<br>EPO; JPO;<br>DERWENT;<br>IBM_TDB | OR               | ON      | 2005/06/15 18:41 |

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OM nucleic - nucleic search, using sw model

Run on: June 20, 2005, 04:54:54 ; Search time 30170 Seconds  
(without alignments)  
11745.210 Million cell updates/sec

Title: US-09-242-772-116

Perfect score: 7313

Sequence: 1 ggcagcgcatacactacaat.....tatgaataaaatctcgtgcc 7313

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:  
1: gb\_ba:  
2: gb\_htg:  
3: gb\_in:  
4: gb\_om:  
5: gb\_ov:  
6: gb\_pat:  
7: gb\_ph:  
8: gb\_pl:  
9: gb\_pr:  
10: gb\_ro:  
11: gb\_sts:  
12: gb\_sy:  
13: gb\_un:  
14: gb\_vi:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result<br>No. | Score | Query |        |        |    | Description |
|---------------|-------|-------|--------|--------|----|-------------|
|               |       | Match | Length | DB     | ID |             |
|               | 1     | 7313  | 100.0  | 7313   | 9  | HSU65002    |
|               | 2     | 7262  | 99.3   | 7313   | 6  | A69511      |
| c             | 3     | 5728  | 78.3   | 142102 | 9  | AC107952    |
|               | 4     | 1514  | 20.7   | 1565   | 9  | BC075047    |
|               | 5     | 1514  | 20.7   | 1565   | 9  | BC075048    |
|               | 6     | 687   | 9.4    | 65748  | 2  | AC090187    |
|               | 7     | 601   | 8.2    | 49357  | 2  | AC107961    |
| c             | 8     | 420   | 5.7    | 65748  | 2  | AC090187    |
| c             | 9     | 406   | 5.6    | 421    | 11 | G25280      |

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|----------|-----|-----|--------|----|----------|--------------------|
| c 10     | 381 | 5.2 | 550    | 9  | AF221550 | AF221550 Homo sapi |
| c 11     | 315 | 4.3 | 376    | 6  | AR274991 | AR274991 Sequence  |
| c 12     | 225 | 3.1 | 274    | 9  | AF221549 | AF221549 Homo sapi |
| c 13     | 177 | 2.4 | 177    | 11 | G33002   | G33002 A009Z02 Hum |
| c 14     | 119 | 1.6 | 524    | 9  | AF221548 | AF221548 Homo sapi |
| c 15     | 117 | 1.6 | 3161   | 10 | AY574219 | AY574219 Mus muscu |
| c 16     | 117 | 1.6 | 182102 | 2  | AC097274 | AC097274 Mus muscu |
| c 17     | 117 | 1.6 | 241148 | 10 | AL807387 | AL807387 Mouse DNA |
| c 18     | 110 | 1.5 | 49357  | 2  | AC107961 | AC107961 Homo sapi |
| c 19     | 100 | 1.4 | 201    | 11 | BV200913 | BV200913 sqnm20538 |
| c 20     | 98  | 1.3 | 135    | 9  | HSU78783 | U78783 Human tumor |
| c 21     | 80  | 1.1 | 278377 | 2  | AC129839 | AC129839 Rattus no |
| c 22     | 78  | 1.1 | 1575   | 10 | AF057366 | AF057366 Mus muscu |
| c 23     | 66  | 0.9 | 244955 | 2  | AC123210 | AC123210 Rattus no |
| c 24     | 60  | 0.8 | 60     | 6  | CQ543597 | CQ543597 Sequence  |
| c 25     | 50  | 0.7 | 1381   | 5  | CR406846 | CR406846 Gallus ga |
| c 26     | 45  | 0.6 | 66     | 11 | HSU84997 | U84997 Homo sapien |
| c 27     | 39  | 0.5 | 107    | 5  | CR353258 | CR353258 Gallus ga |
| c 28     | 36  | 0.5 | 176067 | 10 | AC129040 | AC129040 Rattus no |
| c 29     | 36  | 0.5 | 185673 | 2  | AC141142 | AC141142 Rattus no |
| c 30     | 35  | 0.5 | 660    | 6  | AR502666 | AR502666 Sequence  |
| c 31     | 35  | 0.5 | 660    | 6  | AR517948 | AR517948 Sequence  |
| c 32     | 35  | 0.5 | 160726 | 9  | AC092421 | AC092421 Homo sapi |
| c 33     | 35  | 0.5 | 172947 | 2  | AC068813 | AC068813 Homo sapi |
| c 34     | 35  | 0.5 | 173037 | 2  | AC018542 | AC018542 Homo sapi |
| c 35     | 35  | 0.5 | 179190 | 9  | AC114477 | AC114477 Homo sapi |
| c 36     | 35  | 0.5 | 194609 | 2  | AC013775 | AC013775 Mus muscu |
| c 37     | 35  | 0.5 | 207086 | 10 | AL596117 | AL596117 Mouse DNA |
| c 38     | 35  | 0.5 | 228232 | 2  | AC090293 | AC090293 Mus muscu |
| c 39     | 34  | 0.5 | 728    | 10 | BC031746 | BC031746 Mus muscu |
| c 40     | 34  | 0.5 | 752    | 8  | AY125589 | AY125589 Cylindrot |
| c 41     | 34  | 0.5 | 840    | 3  | AY089459 | AY089459 Drosophil |
| c 42     | 34  | 0.5 | 1900   | 9  | BC071628 | BC071628 Homo sapi |
| c 43     | 34  | 0.5 | 2192   | 5  | BC063223 | BC063223 Xenopus t |
| c 44     | 34  | 0.5 | 3440   | 10 | BC047268 | BC047268 Mus muscu |
| c 45     | 34  | 0.5 | 3911   | 8  | AY639654 | AY639654 Pinus rad |

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OM nucleic - nucleic search, using sw model

Run on: June 20, 2005, 04:37:20 ; Search time 3456 Seconds  
(without alignments)  
12526.351 Million cell updates/sec

Title: US-09-242-772-116

Perfect score: 7313

Sequence: 1 ggcagcgcatacactacaat.....tatgaataaaatctcgtgcc 7313

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:  
1: geneseqn1980s:  
2: geneseqn1990s:  
3: geneseqn2000s:  
4: geneseqn2001as:  
5: geneseqn2001bs:  
6: geneseqn2002as:  
7: geneseqn2002bs:  
8: geneseqn2003as:  
9: geneseqn2003bs:  
10: geneseqn2003cs:  
11: geneseqn2003ds:  
12: geneseqn2004as:  
13: geneseqn2004bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query % | Match | Length | DB       | ID | Description        |
|------------|-------|---------|-------|--------|----------|----|--------------------|
| c 1        | 7262  | 99.3    | 7313  | 2      | AAV29268 |    | Aav29268 Nucleotid |
| c 2        | 315   | 4.3     | 376   | 10     | ADB31412 |    | Adb31412 Testoster |
| c 3        | 117   | 1.6     | 4050  | 12     | ADO35615 |    | Ado35615 Novel mou |
| c 4        | 117   | 1.6     | 24348 | 11     | ACN44976 |    | Acn44976 Mouse gen |
| 5          | 72    | 1.0     | 72    | 4      | AAS13082 |    | Aas13082 DNA encod |
| 6          | 72    | 1.0     | 72    | 8      | ACC41633 |    | Acc41633 Human zin |
| 7          | 60    | 0.8     | 60    | 6      | ABN40484 |    | Abn40484 Human spl |
| 8          | 35    | 0.5     | 24127 | 11     | ACN44540 |    | Acn44540 Mouse gen |
| c 9        | 34    | 0.5     | 540   | 10     | ABX57327 |    | Abx57327 Arabidops |
| 10         | 34    | 0.5     | 3463  | 3      | AAA40241 |    | Aaa40241 Pig heart |

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|----------|----|-----|------|----|----------|--------------------|
| 11       | 33 | 0.5 | 261  | 12 | ADQ18288 | Adq18288 Human sof |
| 12       | 33 | 0.5 | 330  | 12 | ADQ20280 | Adq20280 Human sof |
| c        | 13 | 0.5 | 360  | 6  | ABQ85662 | Abq85662 Arabidops |
| c        | 14 | 0.5 | 372  | 5  | ABV37528 | Abv37528 Human pro |
| c        | 15 | 0.5 | 385  | 10 | ABX61502 | Abx61502 Arabidops |
|          | 16 | 0.5 | 413  | 4  | AAI85388 | Aai85388 Human pol |
|          | 17 | 0.5 | 479  | 13 | ACN52747 | Acn52747 Cotton an |
| c        | 18 | 0.5 | 483  | 13 | ACN47280 | Acn47280 Cotton pr |
|          | 19 | 0.5 | 512  | 9  | ACH26480 | Ach26480 Human adu |
|          | 20 | 0.5 | 523  | 13 | ACN58184 | Acn58184 Cotton gy |
|          | 21 | 0.5 | 945  | 10 | ADL18516 | Adl18516 Rice glut |
|          | 22 | 0.5 | 1034 | 6  | ABK65255 | Abk65255 Arabidops |
|          | 23 | 0.5 | 1034 | 10 | ADD29974 | Add29974 Plant yie |
|          | 24 | 0.5 | 1034 | 12 | ADI41806 | Adi41806 Plant tra |
|          | 25 | 0.5 | 1335 | 3  | AAA47331 | Aaa47331 FtsZ homo |
|          | 26 | 0.5 | 1372 | 12 | ADQ22819 | Adq22819 Human sof |
|          | 27 | 0.5 | 1372 | 12 | ADQ22824 | Adq22824 Human sof |
|          | 28 | 0.5 | 1510 | 4  | AAD08081 | Aad08081 Rice oleo |
|          | 29 | 0.5 | 1832 | 5  | ADL63631 | Adl63631 Human ova |
|          | 30 | 0.5 | 2206 | 4  | ABK43595 | Abk43595 DNA encod |
|          | 31 | 0.5 | 2206 | 12 | ADI53982 | Adi53982 cDNA enco |
|          | 32 | 0.5 | 2385 | 4  | ABL15036 | Ab15036 Drosophil  |
| c        | 33 | 0.5 | 2398 | 3  | AAZ37263 | Aaz37263 SGRF codi |
|          | 34 | 0.5 | 2540 | 6  | ABQ73251 | Abq73251 Human MAP |
|          | 35 | 0.5 | 2823 | 4  | AAS34806 | Aas34806 cDNA enco |
|          | 36 | 0.5 | 2823 | 10 | ADC45964 | Adc45964 Human neo |
|          | 37 | 0.5 | 8447 | 6  | ABN80093 | Abn80093 Human che |
| c        | 38 | 0.4 | 51   | 4  | AAL28293 | Aal28293 Human SNP |
|          | 39 | 0.4 | 163  | 5  | ABV58311 | Abv58311 Human pro |
|          | 40 | 0.4 | 204  | 5  | ABV57555 | Abv57555 Human pro |
|          | 41 | 0.4 | 312  | 5  | ABV49552 | Abv49552 Human pro |
| c        | 42 | 0.4 | 341  | 10 | ABX61217 | Abx61217 Arabidops |
|          | 43 | 0.4 | 348  | 4  | AAI80658 | Aai80658 Human pol |
| c        | 44 | 0.4 | 389  | 5  | ABV61698 | Abv61698 Human pro |
|          | 45 | 0.4 | 397  | 4  | AAI86207 | Aai86207 Human pol |

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OM nucleic - nucleic search, using sw model

Run on: June 20, 2005, 04:06:47 ; Search time 3852 Seconds  
(without alignments)  
11784.990 Million cell updates/sec

Title: US-09-242-772-116

Perfect score: 7313

Sequence: 1 ggcagcgcatacactacaat.....tatgaataaaatctcgtgcc 7313

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 6054689 seqs, 3103772919 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published\_Applications\_NA:\*

1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*

2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*

3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*

4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*

5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*

6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*

7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*

8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*

9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*

10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*

11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*

12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*

13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*

14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*

15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*

16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*

17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*

18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*

19: /cgn2\_6/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*

20: /cgn2\_6/ptodata/2/pubpna/US10H\_PUBCOMB.seq:\*

21: /cgn2\_6/ptodata/2/pubpna/US10I\_PUBCOMB.seq:\*

22: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*

23: /cgn2\_6/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*

24: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*

25: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Page 1

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| Result No. | Score | Query Match | Length | DB    | ID | Description        |
|------------|-------|-------------|--------|-------|----|--------------------|
|            | 1     | 7313        | 100.0  | 7313  | 9  | US-09-242-772-116  |
| c          | 2     | 315         | 4.3    | 376   | 21 | Sequence 116, App  |
| c          | 3     | 117         | 1.6    | 24348 | 13 | Sequence 128, App  |
|            | 4     | 72          | 1.0    | 72    | 9  | Sequence 1693, Ap  |
|            | 5     | 72          | 1.0    | 72    | 16 | Sequence 136, App  |
|            | 6     | 60          | 0.8    | 60    | 10 | Sequence 136, App  |
|            | 7     | 35          | 0.5    | 240   | 18 | Sequence 13232, A  |
| c          | 8     | 35          | 0.5    | 671   | 20 | Sequence 118528, A |
|            | 9     | 35          | 0.5    | 735   | 20 | Sequence 64671, A  |
|            | 10    | 35          | 0.5    | 3112  | 20 | Sequence 17914, A  |
|            | 11    | 35          | 0.5    | 24127 | 13 | Sequence 51136, A  |
|            | 12    | 34          | 0.5    | 470   | 19 | Sequence 1039, Ap  |
| c          | 13    | 34          | 0.5    | 540   | 9  | Sequence 45935, A  |
| c          | 14    | 34          | 0.5    | 2124  | 18 | Sequence 679, App  |
|            | 15    | 33          | 0.5    | 197   | 20 | Sequence 3238, Ap  |
|            | 16    | 33          | 0.5    | 261   | 20 | Sequence 36720, A  |
|            | 17    | 33          | 0.5    | 270   | 19 | Sequence 1106, Ap  |
|            | 18    | 33          | 0.5    | 282   | 20 | Sequence 6529, Ap  |
|            | 19    | 33          | 0.5    | 330   | 20 | Sequence 134998, A |
| c          | 20    | 33          | 0.5    | 345   | 20 | Sequence 3100, Ap  |
| c          | 21    | 33          | 0.5    | 360   | 9  | Sequence 31440, A  |
| c          | 22    | 33          | 0.5    | 372   | 20 | Sequence 532, App  |
|            | 23    | 33          | 0.5    | 375   | 20 | Sequence 37547, A  |
|            | 24    | 33          | 0.5    | 380   | 20 | Sequence 165833, A |
|            | 25    | 33          | 0.5    | 384   | 18 | Sequence 57654, A  |
| c          | 26    | 33          | 0.5    | 385   | 9  | Sequence 58174, A  |
| c          | 27    | 33          | 0.5    | 392   | 20 | Sequence 848, App  |
| c          | 28    | 33          | 0.5    | 402   | 18 | Sequence 65919, A  |
|            | 29    | 33          | 0.5    | 422   | 20 | Sequence 76918, A  |
| c          | 30    | 33          | 0.5    | 427   | 20 | Sequence 89893, A  |
|            | 31    | 33          | 0.5    | 430   | 20 | Sequence 4382, Ap  |
| c          | 32    | 33          | 0.5    | 458   | 19 | Sequence 58879, A  |
| c          | 33    | 33          | 0.5    | 465   | 19 | Sequence 86639, A  |
|            | 34    | 33          | 0.5    | 479   | 19 | Sequence 34432, A  |
| c          | 35    | 33          | 0.5    | 483   | 19 | Sequence 7528, Ap  |
| c          | 36    | 33          | 0.5    | 484   | 18 | Sequence 2061, Ap  |
|            | 37    | 33          | 0.5    | 512   | 10 | Sequence 92471, A  |
|            | 38    | 33          | 0.5    | 523   | 19 | Sequence 13692, A  |
| c          | 39    | 33          | 0.5    | 570   | 20 | Sequence 12965, A  |
| c          | 40    | 33          | 0.5    | 626   | 20 | Sequence 48090, A  |
| c          | 41    | 33          | 0.5    | 637   | 20 | Sequence 14398, A  |
| c          | 42    | 33          | 0.5    | 690   | 20 | Sequence 33996, A  |
|            | 43    | 33          | 0.5    | 715   | 21 | Sequence 164109, A |
|            | 44    | 33          | 0.5    | 715   | 21 | Sequence 3705, Ap  |
| c          | 45    | 33          | 0.5    | 787   | 20 | Sequence 8940, Ap  |
|            |       |             |        |       |    | Sequence 126784, A |

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OM nucleic - nucleic search, using sw model

Run on: June 20, 2005, 01:23:31 ; Search time 3482 Seconds  
(without alignments)  
9277.886 Million cell updates/sec

Title: US-09-242-772-116

Perfect score: 7313

Sequence: 1 ggcagcgcatacactacaat.....tatgaataaaatctcgtgcc 7313

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 12999316 seqs, 2208778887 residues

word size : 0

Total number of hits satisfying chosen parameters: 25998632

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending\_Patents\_NA\_New:\*

1: /cgn2\_6/ptodata/2/pna/PCT\_NEW\_COMB.seq:\*

2: /cgn2\_6/ptodata/2/pna/PCT\_NEW\_COMB.seq2:\*

3: /cgn2\_6/ptodata/2/pna/US06\_NEW\_COMB.seq:\*

4: /cgn2\_6/ptodata/2/pna/US07\_NEW\_COMB.seq:\*

5: /cgn2\_6/ptodata/2/pna/US08\_NEW\_COMB.seq:\*

6: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq:\*

7: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq:\*

8: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq2:\*

9: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq3:\*

10: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq4:\*

11: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq5:\*

12: /cgn2\_6/ptodata/2/pna/US11\_NEW\_COMB.seq:\*

13: /cgn2\_6/ptodata/2/pna/US11\_NEW\_COMB.seq2:\*

14: /cgn2\_6/ptodata/2/pna/US11\_NEW\_COMB.seq3:\*

15: /cgn2\_6/ptodata/2/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query |        | DB | ID                    | Description       |
|------------|-------|-------|--------|----|-----------------------|-------------------|
|            |       | Match | %      |    |                       |                   |
| 1          | 563   | 7.7   | 4174   | 15 | US-60-680-544-32916   | Sequence 32916, A |
| 2          | 563   | 7.7   | 4174   | 15 | US-60-680-473-32916   | Sequence 32916, A |
| 3          | 35    | 0.5   | 760    | 9  | US-10-703-032-103073  | Sequence 103073,  |
| c 4        | 34    | 0.5   | 601    | 11 | US-10-940-774A-28962  | Sequence 28962, A |
| c 5        | 34    | 0.5   | 601    | 11 | US-10-940-774A-125909 | Sequence 125909,  |
| c 6        | 34    | 0.5   | 115963 | 11 | US-10-940-774A-12298  | Sequence 12298, A |
| c 7        | 34    | 0.5   | 144322 | 11 | US-10-940-774A-15316  | Sequence 15316, A |
| c 8        | 34    | 0.5   | 152321 | 15 | US-60-659-397-12128   | Sequence 12128, A |

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|      |    |     |        |    |                       |                   |
|------|----|-----|--------|----|-----------------------|-------------------|
| c 9  | 33 | 0.5 | 201    | 11 | US-10-990-328A-541037 | Sequence 541037,  |
| c 10 | 33 | 0.5 | 400    | 9  | US-10-703-032-73280   | Sequence 73280, A |
| c 11 | 33 | 0.5 | 400    | 9  | US-10-703-032-99398   | Sequence 99398, A |
| c 12 | 33 | 0.5 | 450    | 9  | US-10-703-032-79323   | Sequence 79323, A |
| c 13 | 33 | 0.5 | 456    | 9  | US-10-703-032-70659   | Sequence 70659, A |
| c 14 | 33 | 0.5 | 496    | 9  | US-10-703-032-88434   | Sequence 88434, A |
| c 15 | 33 | 0.5 | 601    | 11 | US-10-940-774A-115142 | Sequence 115142,  |
| c 16 | 33 | 0.5 | 696    | 9  | US-10-703-032-13726   | Sequence 13726, A |
| c 17 | 33 | 0.5 | 732    | 9  | US-10-703-032-12833   | Sequence 12833, A |
| c 18 | 33 | 0.5 | 766    | 9  | US-10-703-032-17311   | Sequence 17311, A |
| 19   | 33 | 0.5 | 1034   | 6  | US-09-713-994A-1780   | Sequence 1780, Ap |
| 20   | 33 | 0.5 | 1747   | 7  | US-10-062-254A-357    | Sequence 357, App |
| 21   | 33 | 0.5 | 2385   | 12 | US-11-097-143-19795   | Sequence 19795, A |
| 22   | 33 | 0.5 | 11730  | 11 | US-10-940-774A-14991  | Sequence 14991, A |
| 23   | 33 | 0.5 | 29571  | 15 | US-60-659-397-12103   | Sequence 12103, A |
| c 24 | 33 | 0.5 | 49416  | 11 | US-10-940-774A-15234  | Sequence 15234, A |
| c 25 | 33 | 0.5 | 93364  | 11 | US-10-940-774A-14890  | Sequence 14890, A |
| 26   | 33 | 0.5 | 151541 | 11 | US-10-990-328A-97855  | Sequence 97855, A |
| 27   | 33 | 0.5 | 283538 | 11 | US-10-940-774A-13506  | Sequence 13506, A |
| 28   | 33 | 0.5 | 401433 | 2  | PCT-US04-42189-79     | Sequence 79, Appl |
| c 29 | 33 | 0.5 | 474412 | 11 | US-10-990-328A-98016  | Sequence 98016, A |
| 30   | 33 | 0.5 | 483207 | 1  | PCT-US04-37982-3303   | Sequence 3303, Ap |
| c 31 | 32 | 0.4 | 51     | 6  | US-09-749-280D-1501   | Sequence 1501, Ap |
| c 32 | 32 | 0.4 | 201    | 11 | US-10-990-328A-215196 | Sequence 215196,  |
| c 33 | 32 | 0.4 | 201    | 11 | US-10-990-328A-215230 | Sequence 215230,  |
| 34   | 32 | 0.4 | 201    | 11 | US-10-990-328A-234783 | Sequence 234783,  |
| 35   | 32 | 0.4 | 201    | 11 | US-10-990-328A-234784 | Sequence 234784,  |
| 36   | 32 | 0.4 | 446    | 9  | US-10-703-032-3773    | Sequence 3773, Ap |
| c 37 | 32 | 0.4 | 525    | 15 | US-60-680-544-3950    | Sequence 3950, Ap |
| 38   | 32 | 0.4 | 525    | 15 | US-60-680-544-14578   | Sequence 14578, A |
| c 39 | 32 | 0.4 | 525    | 15 | US-60-680-473-3950    | Sequence 3950, Ap |
| 40   | 32 | 0.4 | 525    | 15 | US-60-680-473-14578   | Sequence 14578, A |
| 41   | 32 | 0.4 | 564    | 9  | US-10-703-032-57200   | Sequence 57200, A |
| 42   | 32 | 0.4 | 600    | 13 | US-11-060-756-278     | Sequence 278, App |
| 43   | 32 | 0.4 | 600    | 13 | US-11-060-756-4550    | Sequence 4550, Ap |
| 44   | 32 | 0.4 | 784    | 7  | US-10-456-882A-40     | Sequence 40, Appl |
| 45   | 32 | 0.4 | 830    | 15 | US-60-680-544-17295   | Sequence 17295, A |

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 20, 2005, 11:48:05 ; Search time 21091 Seconds  
(without alignments)  
13198.236 Million cell updates/sec

Title: US-09-242-772-116

Perfect score: 7313

Sequence: 1 ggcagcgcatacactacaat.....tatgaataaaatctcgtgcc 7313

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_htc:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gss1:\*

9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID       | Description        |
|------------|-------|-------------|--------|----|----------|--------------------|
| 1          | 1452  | 19.9        | 1503   | 9  | AY420150 | AY420150 Homo sapi |
| 2          | 685   | 9.4         | 693    | 4  | BM724590 | BM724590 UI-E-E01- |
| 3          | 679   | 9.3         | 1503   | 9  | AY420151 | AY420151 Pan trogl |
| c 4        | 637   | 8.7         | 742    | 6  | CA413047 | CA413047 UI-H-EZ0- |
| c 5        | 596   | 8.1         | 864    | 5  | BX370812 | BX370812 BX370812  |
| c 6        | 583   | 8.0         | 583    | 5  | BP317766 | BP317766 BP317766  |
| c 7        | 570   | 7.8         | 570    | 2  | AW339499 | AW339499 xz91g05.x |
| c 8        | 548   | 7.5         | 734    | 6  | CA411972 | CA411972 UI-H-EZ0- |
| c 9        | 541   | 7.4         | 616    | 5  | BU686683 | BU686683 UI-CF-DU1 |
| c 10       | 540   | 7.4         | 540    | 1  | AA706806 | AA706806 zj30c09.s |
| c 11       | 518   | 7.1         | 518    | 2  | BF115791 | BF115791 7n64h11.x |
| 12         | 514   | 7.0         | 1047   | 5  | BX402039 | BX402039 BX402039  |
| 13         | 497   | 6.8         | 500    | 2  | BF507694 | BF507694 UI-H-BW1- |
| 14         | 497   | 6.8         | 736    | 1  | AL036879 | AL036879 DKFZp564P |

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|      |     |     |      |   |          |          |            |
|------|-----|-----|------|---|----------|----------|------------|
| c 15 | 487 | 6.7 | 1165 | 5 | BX424854 | BX424854 | BX424854   |
| c 16 | 482 | 6.6 | 482  | 1 | AA707386 | AA707386 | zj27e09.s  |
| 17   | 475 | 6.5 | 790  | 1 | AU138448 | AU138448 | AU138448   |
| c 18 | 464 | 6.3 | 466  | 1 | AA628501 | AA628501 | af27d06.s  |
| 19   | 461 | 6.3 | 909  | 5 | BU181917 | BU181917 | AGENCOURT  |
| c 20 | 459 | 6.3 | 467  | 2 | AW274762 | AW274762 | xn34h01.x  |
| c 21 | 448 | 6.1 | 597  | 2 | AW977860 | AW977860 | EST389864  |
| 22   | 439 | 6.0 | 449  | 6 | CA771364 | CA771364 | io70c07.y  |
| 23   | 438 | 6.0 | 907  | 4 | BG613583 | BG613583 | 602641935  |
| c 24 | 430 | 5.9 | 432  | 2 | BF432133 | BF432133 | nab79g01.  |
| 25   | 426 | 5.8 | 536  | 7 | CN410058 | CN410058 | 170004245  |
| c 26 | 423 | 5.8 | 423  | 1 | AI334157 | AI334157 | qq07h12.x  |
| c 27 | 409 | 5.6 | 458  | 2 | AW002999 | AW002999 | wq62d08.x  |
| c 28 | 409 | 5.6 | 560  | 1 | AI808840 | AI808840 | wt97h04.x  |
| c 29 | 406 | 5.6 | 421  | 7 | D59273   | D59273   | HUM007A10A |
| c 30 | 373 | 5.1 | 373  | 1 | AA418372 | AA418372 | zv96g12.r  |
| c 31 | 373 | 5.1 | 494  | 2 | AW007402 | AW007402 | wt55b04.x  |
| 32   | 371 | 5.1 | 569  | 5 | BP379355 | BP379355 | BP379355   |
| c 33 | 353 | 4.8 | 427  | 1 | AI223324 | AI223324 | qg71c02.x  |
| c 34 | 347 | 4.7 | 391  | 7 | N95376   | N95376   | zb71f10.s1 |
| 35   | 320 | 4.4 | 460  | 1 | AV745206 | AV745206 | AV745206   |
| c 36 | 315 | 4.3 | 673  | 9 | AG120959 | AG120959 | Pan trogl  |
| 37   | 310 | 4.2 | 514  | 7 | CN410057 | CN410057 | 170005830  |
| 38   | 305 | 4.2 | 467  | 7 | T83418   | T83418   | yd44d05.r1 |
| 39   | 299 | 4.1 | 410  | 7 | CN410056 | CN410056 | 170005325  |
| 40   | 288 | 3.9 | 319  | 2 | AW138020 | AW138020 | UI-H-BI1-  |
| c 41 | 285 | 3.9 | 517  | 7 | T81600   | T81600   | yd44d05.s1 |
| 42   | 284 | 3.9 | 489  | 1 | AV745506 | AV745506 | AV745506   |
| 43   | 261 | 3.6 | 454  | 1 | AA418251 | AA418251 | zv96c12.s  |
| 44   | 259 | 3.5 | 259  | 1 | AA421591 | AA421591 | zu25f01.r  |
| 45   | 249 | 3.4 | 922  | 4 | BG253502 | BG253502 | 602364227  |